

CLAIM AMENDMENTS

1-31. (canceled)

32. (currently amended): A method of detecting gene silencing of a target gene in a mammalian organism or in cellular material of a mammalian organism which method comprises the steps of: detecting in a nucleic acid extract prepared from said organism or in cellular material from said organism the presence as opposed to the absence of short RNA molecules (SRMs) of uniform length which are 20-30 nucleotides in length in said extract, characterizing any SRMs which are present in said extract wherein said characterizing comprises determining sequence identity or similarity with said target gene, wherein the presence of any SRMs having identity or similarity with said target gene indicates silencing of said target gene in the organism or in cellular material from said organism, and confirming that said target gene has been silenced.

33-35. (canceled)

36. (previously presented): The method of claim 32, wherein the SRMs are short antisense RNA molecules (SARMs).

37. (previously presented): The method of claim 32, wherein the SRMs are short sense RNA molecules (SSRMs).

38-40. (canceled)

41. (previously presented): The method of claim 32, wherein the step of characterizing any SRMs present in the extract to determine sequence identity or similarity with a target gene is performed by a process that comprises: tagging said SRMs with a marker, probing a library of genes from said organism, and identifying the genes in said library that bind to said SRMs whereby a gene that binds to said SRM is identified as said target gene which is silenced.

42-48. (canceled)

49. (previously presented): The method of claim 32, wherein said short RNA molecules are 20-25 nucleotides in length.

50-66. (canceled)

67. (previously presented): The method of claim 32, wherein the SRMs comprise both short antisense RNA molecules (SARMs) and short sense RNA molecules (SSRMs).

68. (previously presented): The method of claim 32, wherein said characterizing comprises determining sequence identity with the target.

69. (canceled)

70. (currently amended): The method of claim 32, wherein as a result of said characterizing, sequences of SRMs are correlated with the occurrence of gene silencing in said mammalian organism or in cellular material from said organism.

71. (previously presented): The method of claim 32, wherein said SRMs are 20 nucleotides in length.

72. (previously presented): The method of claim 32, wherein said SRMs are 21 nucleotides in length.

73. (previously presented): The method of claim 32, wherein said SRMs are 22 nucleotides in length.

74. (previously presented): The method of claim 32, wherein said SRMs are 23 nucleotides in length.

75. (previously presented): The method of claim 32, wherein said SRMs are 24 nucleotides in length.

76. (previously presented): The method of claim 32, wherein said SRMs are 25 nucleotides in length.

77. (previously presented): The method of claim 32, wherein said SRMs are 26 nucleotides in length.

78. (previously presented): The method of claim 32, wherein said SRMs are 27 nucleotides in length.

79. (previously presented): The method of claim 32, wherein said SRMs are 28 nucleotides in length.

80. (previously presented): The method of claim 32, wherein said SRMs are 29 nucleotides in length.

81. (previously presented): The method of claim 32, wherein said SRMs are 30 nucleotides in length.

82-83. (canceled)